RAW SEQUENCE LISTING

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Application Serial Number: __10/578,613__

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PATENT APPLICATION: US/10/578,613   TIME: 14:57:33

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 3 <110> APPLICANT: Tohata, Masatoshi
 4        Sawada, Kazuhisa
 5        Ozaki, Katsuya
 6        Kobayashi, Kazuo
 7        Ogasawara, Naotake
 9 <120> TITLE OF INVENTION: RECOMBINANT MICROORGANISM
11 <130> FILE REFERENCE: 289779US0PCT
13 <140> CURRENT APPLICATION NUMBER: 10/578,613
14 <141> CURRENT FILING DATE: 2006-05-08
16 <150> PRIOR APPLICATION NUMBER: PCT/JP04/16891
17 <151> PRIOR FILING DATE: 2004-11-05
19 <150> PRIOR APPLICATION NUMBER: JP 2003-379167
20 <151> PRIOR FILING DATE: 2003-11-07
22 <160> NUMBER OF SEQ ID NOS: 122
24 <170> SOFTWARE: PatentIn version 3.3
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45 gaaataaaag tagaagacaa aggacataag aaaattgcat tagttttaat tatagaaaac      180
47 gccttttat aattatttat acctagaacg aaaatactgt ttcgaaagcg gtttactata      240
49 aaaccttata ttccggctct tttttaaaac aggggtaaa aattcactct agtattctaa      300
51 tttcaacatg ctataataaa tttgtaagac gcaatatgca tctctttttt tacgatatat      360
53 gtaagcggtt aaccttgtgc tatatgccga tttaggaagg ggggtagatt gagtcaagta      420
55 gtaataatat agataactta taagttgttg agaagcagga gagcatctgg gttactcaca      480
57 agttttttta aaactttaac gaaagcactt tcggtaatgc ttatgaattt agctatttga      540
59 ttcaattact ttaaaaatat ttaggaggta at atg atg tta aga aag aaa aca       593
60                                       Met Met Leu Arg Lys Lys Thr
61                                       1               5
63 aag cag ttg att tct tcc att ctt att tta gtt tta ctt cta tct tta       641
64 Lys Gln Leu Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Leu Ser Leu
65         10              15                  20
67 ttt ccg gca gct ctt gca gca gaa gga aac act cgt gaa gac aat ttt       689
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71 aaa cat tta tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc      737
72 Lys His Leu Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly
73 40                      45                    50                    55
75 gca tta caa tta caa gaa gtc gat gga caa atg aca tta gta gat caa      785
76 Ala Leu Gln Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln
77                      60                    65                    70
79 cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag      833
80 His Gly Glu Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln
81              75                    80                    85
83 tgg ttt cct gag atc ttg aat gat aac gca tac aaa gct ctt tct aac      881
84 Trp Phe Pro Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn
85          90                    95                    100
87 gat tgg gat tcc aat atg att cgt ctt gct atg tat gta ggt gaa aat      929
88 Asp Trp Asp Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn
89      105                    110                    115
91 ggg tac gct aca aac cct gag tta atc aaa caa aga gtg att gat gga      977
92 Gly Tyr Ala Thr Asn Pro Glu Leu Ile Lys Gln Arg Val Ile Asp Gly
93 120                    125                    130                    135
95 att gag tta gcg att gaa aat gac atg tat gtt att gtt gac tgg cat     1025
96 Ile Glu Leu Ala Ile Glu Asn Asp Met Tyr Val Ile Val Asp Trp His
97                    140                    145                    150
99 gtt cat gcg cca ggt gat cct aga gat cct gtt tat gca ggt gct aaa     1073
100 Val His Ala Pro Gly Asp Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys
101                  155                    160                    165
103 gat ttc ttt aga gaa att gca gct tta tac cct aat aat cca cac att     1121
104 Asp Phe Phe Arg Glu Ile Ala Ala Leu Tyr Pro Asn Asn Pro His Ile
105            170                    175                    180
107 att tat gag tta gcg aat gag ccg agt agt aat aat aat ggt gga gca     1169
108 Ile Tyr Glu Leu Ala Asn Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala
109      185                    190                    195
111 ggg att ccg aat aac gaa gaa ggt tgg aaa gcg gta aaa gaa tat gct     1217
112 Gly Ile Pro Asn Asn Glu Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala
113 200                    205                    210                    215
115 gat cca att gta gaa atg tta cgt aaa agc ggt aat gca gat gac aac     1265
116 Asp Pro Ile Val Glu Met Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn
117                  220                    225                    230
119 att atc att gtt ggt agt cca aac tgg agt cag cgt ccg gac tta gca     1313
120 Ile Ile Ile Val Gly Ser Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala
121            235                    240                    245
123 gct gat aat cca att gat gat cac cat aca atg tat act gtt cac ttc     1361
124 Ala Asp Asn Pro Ile Asp Asp His His Thr Met Tyr Thr Val His Phe
125            250                    255                    260
127 tac act ggt tca cat gct gct tca act gaa agc tat ccg tct gaa act     1409
128 Tyr Thr Gly Ser His Ala Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr
129      265                    270                    275
131 cct aac tct gaa aga gga aac gta atg agt aac act cgt tat gcg tta     1457
132 Pro Asn Ser Glu Arg Gly Asn Val Met Ser Asn Thr Arg Tyr Ala Leu
133 280                    285                    290                    295
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136 Glu Asn Gly Val Ala Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala
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139 agt gga gac ggt ggt cct tac ttt gat gaa gca gat gta tgg att gaa    1553
140 Ser Gly Asp Gly Gly Pro Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu
141             315                     320                 325
143 ttt tta aat gaa aac aac att agc tgg gct aac tgg tct tta acg aat    1601
144 Phe Leu Asn Glu Asn Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn
145             330                     335                 340
147 aaa aat gaa gta tct ggt gca ttt aca cca ttc gag tta ggt aag tct    1649
148 Lys Asn Glu Val Ser Gly Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser
149     345                 350                     355
151 aac gca acc aat ctt gac cca ggt cca gat cat gtg tgg gca cca gaa    1697
152 Asn Ala Thr Asn Leu Asp Pro Gly Pro Asp His Val Trp Ala Pro Glu
153 360                 365                     370                 375
155 gaa tta agt ctt tct gga gaa tat gta cgt gct cgt att aaa ggt gtg    1745
156 Glu Leu Ser Leu Ser Gly Glu Tyr Val Arg Ala Arg Ile Lys Gly Val
157             380                     385                 390
159 aac tat gag cca atc gac cgt aca aaa tac acg aaa gta ctt tgg gac    1793
160 Asn Tyr Glu Pro Ile Asp Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp
161             395                     400                 405
163 ttt aat gat gga acg aag caa gga ttt gga gtg aat tcg gat tct cca    1841
164 Phe Asn Asp Gly Thr Lys Gln Gly Phe Gly Val Asn Ser Asp Ser Pro
165             410                     415                 420
167 aat aaa gaa ctt att gca gtt gat aat gaa aac aac act ttg aaa gtt    1889
168 Asn Lys Glu Leu Ile Ala Val Asp Asn Glu Asn Asn Thr Leu Lys Val
169     425                 430                     435
171 tcg gga tta gat gta agt aac gat gtt tca gat ggc aac ttc tgg gct    1937
172 Ser Gly Leu Asp Val Ser Asn Asp Val Ser Asp Gly Asn Phe Trp Ala
173 440                 445                     450                 455
175 aat gct cgt ctt tct gcc aac ggt tgg gga aaa agt gtt gat att tta    1985
176 Asn Ala Arg Leu Ser Ala Asn Gly Trp Gly Lys Ser Val Asp Ile Leu
177             460                     465                 470
179 ggt gct gag aag ctt aca atg gat gtt att gtt gat gaa cca acg acg    2033
180 Gly Ala Glu Lys Leu Thr Met Asp Val Ile Val Asp Glu Pro Thr Thr
181             475                     480                 485
183 gta gct att gcg gcg att cca caa agt agt aaa agt gga tgg gca aat    2081
184 Val Ala Ile Ala Ala Ile Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn
185             490                     495                 500
187 cca gag cgt gct gtt cga gtg aac gcg gaa gat ttt gtc cag caa acg    2129
188 Pro Glu Arg Ala Val Arg Val Asn Ala Glu Asp Phe Val Gln Gln Thr
189     505                 510                     515
191 gac ggt aag tat aaa gct gga tta aca att aca gga gaa gat gct cct    2177
192 Asp Gly Lys Tyr Lys Ala Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro
193 520                 525                     530                 535
195 aac cta aaa aat atc gct ttt cat gaa gaa gat aac aat atg aac aac    2225
196 Asn Leu Lys Asn Ile Ala Phe His Glu Glu Asp Asn Asn Met Asn Asn
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200 Ile Ile Leu Phe Val Gly Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp
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204 Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile Pro Val Val His Asp
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207 cca aaa gga gaa gct gtt ctt cct tct gtt ttt gaa gac ggt aca cgt    2369
208 Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe Glu Asp Gly Thr Arg
209         585                 590                 595
211 caa ggt tgg gac tgg gct gga gag tct ggt gtg aaa aca gct tta aca    2417
212 Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val Lys Thr Ala Leu Thr
213 600                 605                 610                 615
215 att gaa gaa gca aac ggt tct aac gcg tta tca tgg gaa ttt gga tat    2465
216 Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr
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220 Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp
221         635                 640                 645
223 ttc tgg aaa tct gac ttg gtt cgc ggt gag aat gat tat gta gct ttt    2561
224 Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn Asp Tyr Val Ala Phe
225         650                 655                 660
227 gat ttc tat cta gat cca gtt cgt gca aca gaa ggc gca atg aat atc    2609
228 Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu Gly Ala Met Asn Ile
229         665                 670                 675
231 aat tta gta ttc cag cca cct act aac ggg tat tgg gta caa gca cca    2657
232 Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro
233 680                 685                 690                 695
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236 Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu Glu Ala Asn Gln Val
237         700                 705                 710
239 aat ggt tta tat cac tat gaa gtg aaa att aac gta aga gat att aca    2753
240 Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn Val Arg Asp Ile Thr
241         715                 720                 725
243 aac att caa gat gac acg tta cta cgt aac atg atg atc att ttt gca    2801
244 Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met Met Ile Ile Phe Ala
245         730                 735                 740
247 gat gta gaa agt gac ttt gca ggg aga gtc ttt gta gat aat gtt cgt    2849
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251 ttt gag ggg gct gct act act gag ccg gtt gaa cca gag cca gtt gat    2897
252 Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu Pro Glu Pro Val Asp
253 760                 765                 770                 775
255 cct ggc gaa gag acg cca cct gtc gat gag aag gaa gcg aaa aaa gaa    2945
256 Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu
257         780                 785                 790
259 caa aaa gaa gca gag aaa gaa gag aaa gaa gca gta aaa gaa gaa aag    2993
260 Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala Val Lys Glu Glu Lys
261         795                 800                 805
263 aaa gaa gct aaa gaa gaa aag aaa gca gtc aaa aat gag gct aag aaa    3041
264 Lys Glu Ala Lys Glu Glu Lys Lys Ala Val Lys Asn Glu Ala Lys Lys
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276 <212> TYPE: PRT
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286             20                  25                 30
289 Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val
290             35                  40                 45
293 Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly
294     50                  55                 60
297 Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly
298 65                  70                 75                 80
301 Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn
302             85                  90                 95
305 Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu
306             100                 105                110
309 Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile
310             115                 120                125
313 Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met
314     130                 135                140
317 Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp
318 145                 150                 155                160
321 Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu
322             165                 170                175
325 Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser
326             180                 185                190
329 Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp
330             195                 200                205
333 Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys
334     210                 215                220
337 Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp
338 225                 230                 235                240
341 Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His
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346             260                 265                270
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350             275                 280                285
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Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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